Ubap2l Cas9-KO Strategy

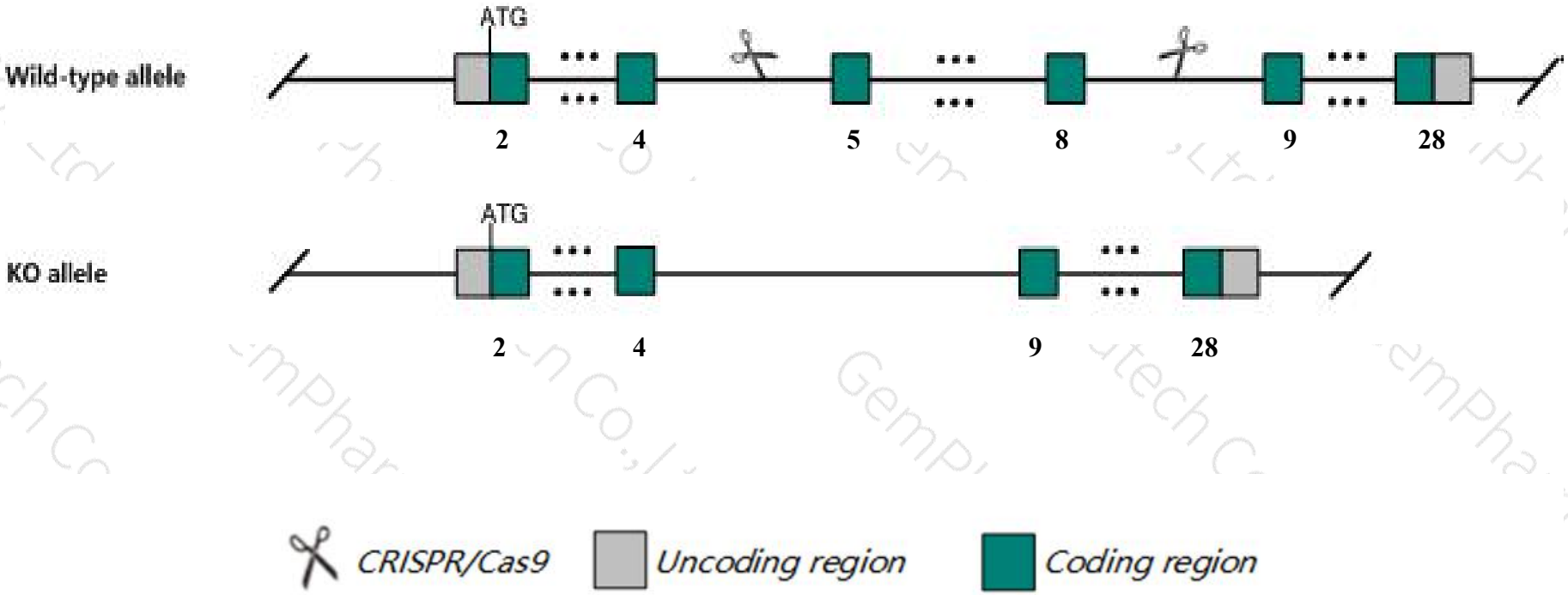
Designer: Huimin Su

Project Overview

Project Name	***Ubap2l***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Ubap2l* gene. The schematic diagram is as follows:



Technical routes

➢ The *Ubap2l* gene has 23 transcripts. According to the structure of *Ubap2l* gene, exon5-exon8 of *Ubap2l-202* (ENSMUST00000064639.14) transcript is recommended as the knockout region. The region contains 424bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Ubap2l* gene. The brief process is as follows: gRNA was transcribed in vitro.Cas9 and gRNA were microinjected into the fertilized eggs of C57BL/6JGpt mice. Fertilized eggs were transplanted to obtain positive F0 mice which were confirmed by PCR and sequencing. A stable F1 generation mouse model was obtained by mating positive F0 generation mice with C57BL/6JGpt mice.

Notice

- According to the existing MGI data,Mice homozygous for a transgenic gene disruption exhibit decreased female body size and reduced female fertility.
- The transcripts *Ubap2l-213, Ubap2l-211, Ubap2l-221, Ubap2l-209* and *Ubap2l-217* are incomplete, so the effect on them are unknown.
- The *Ubap2l* gene is located on the Chr3. If the knockout mice are crossed with other mice strains to obtain double gene positive homozygous mouse offspring, please avoid the two genes on the same chromosome.
- This Strategy is designed based on genetic information in existing databases. Due to the complexity of gene transcription and translation processes, all risks cannot be predicted under existing information.

Gene information（NCBI）

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Ubap2l ubiquitin-associated protein 2-like [Mus musculus (house mouse)]

Gene ID: 74383, updated on 31-Jan-2019

Summary

Official Symbol	Ubap2l provided by MGI
Official Full Name	ubiquitin-associated protein 2-like provided byMGI
Primary source	MGI:MGI:1921633
See related	Ensembl:ENSMUSG00000042520
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	3110083O19Rik, 4932431F02Rik, A430103N23Rik, C77168, Nice-4, mKIAA0144
Expression	Ubiquitous expression in limb E14.5 (RPKM 19.2), testis adult (RPKM 17.9) and 28 other tissuesSee more
Orthologs	human all

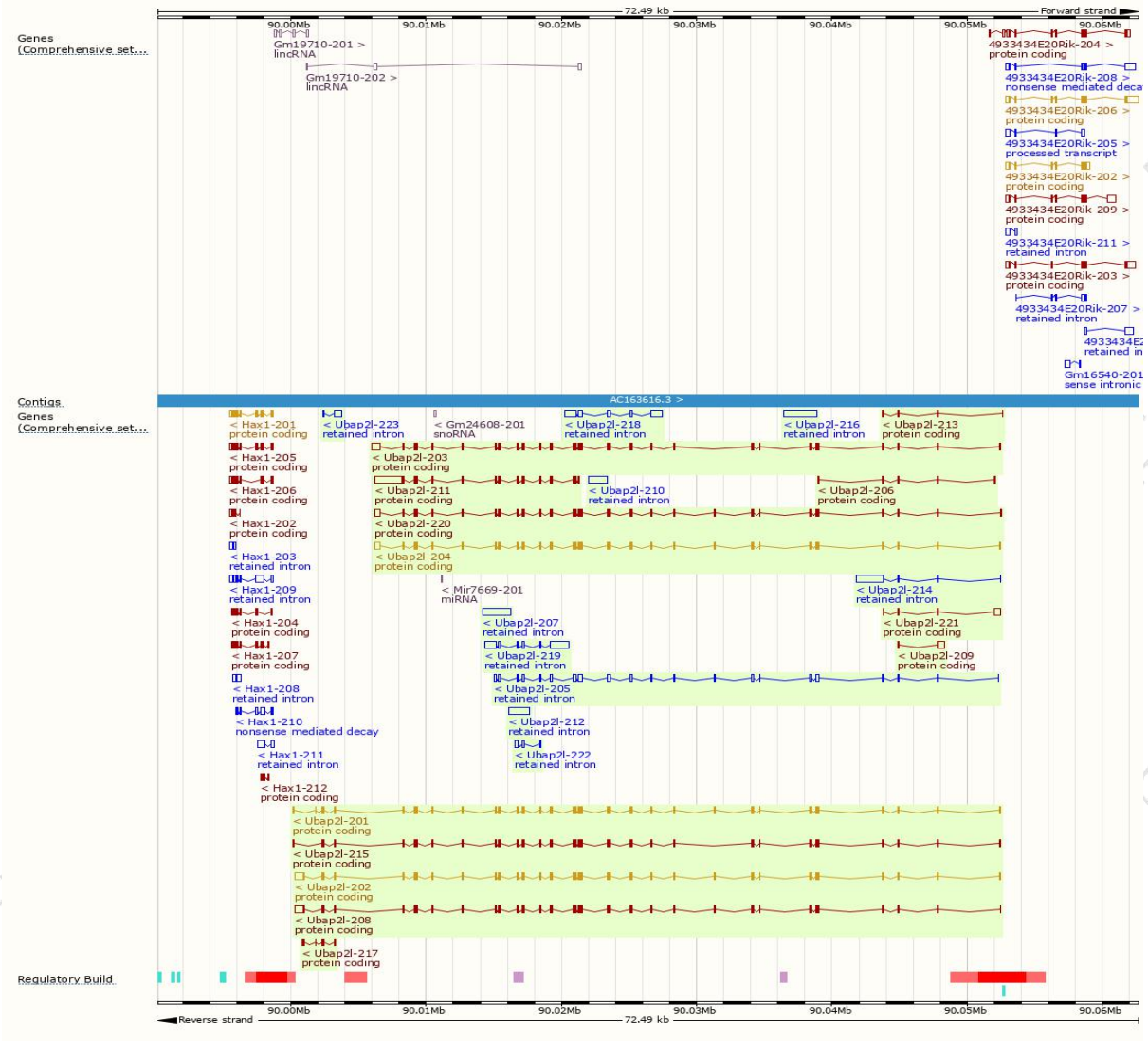
Transcript information（Ensembl）

The gene has 23 transcripts,all transcripts are shown below:

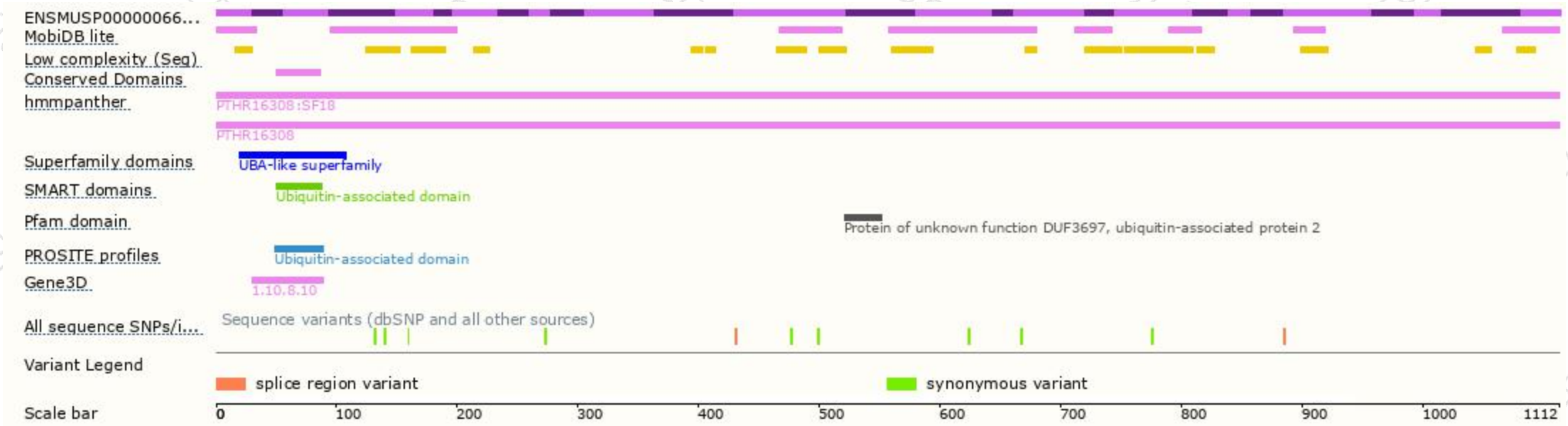
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Ubap2l-202	ENSMUST00000064639.14	4073	1112aa	Protein coding	CCDS50966	Q80X50	TSL:1 GENCODE basic
Ubap2l-208	ENSMUST00000196843.4	3975	1107aa	Protein coding	CCDS79960	Q80X50	TSL:5 GENCODE basic
Ubap2l-203	ENSMUST00000090908.10	3629	983aa	Protein coding	CCDS79959	A0A0H2UH17	TSL:1 GENCODE basic APPRIS ALT1
Ubap2l-204	ENSMUST00000195995.4	3516	1014aa	Protein coding	CCDS50965	Q80X50	TSL:1 GENCODE basic APPRIS P3
Ubap2l-201	ENSMUST00000029553.15	3509	1105aa	Protein coding	CCDS38498	Q80X50	TSL:1 GENCODE basic
Ubap2l-220	ENSMUST00000199834.4	3494	1014aa	Protein coding	CCDS50965	Q80X50	TSL:1 GENCODE basic APPRIS P3
Ubap2l-215	ENSMUST00000198322.4	3385	1067aa	Protein coding	CCDS79958	A0A0G2JDV6	TSL:1 GENCODE basic APPRIS ALT1
Ubap2l-211	ENSMUST00000197177.4	3503	497aa	Protein coding	-	A0A0G2JFN7	CDS 5' incomplete TSL:1
Ubap2l-221	ENSMUST00000199929.1	623	57aa	Protein coding	-	A0A0G2JDT1	CDS 3' incomplete TSL:2
Ubap2l-209	ENSMUST00000196917.1	592	50aa	Protein coding	-	A0A0G2JE24	CDS 3' incomplete TSL:3
Ubap2l-217	ENSMUST00000199050.1	473	129aa	Protein coding	-	A0A0G2JEC6	CDS 5' incomplete TSL:3
Ubap2l-206	ENSMUST00000196633.4	410	105aa	Protein coding	-	A0A0G2JG47	CDS 3' incomplete TSL:3
Ubap2l-213	ENSMUST00000197903.4	328	81aa	Protein coding	-	A0A0G2JGD0	CDS 3' incomplete TSL:3
Ubap2l-219	ENSMUST00000199612.4	2789	No protein	Retained intron	-	-	TSL:1
Ubap2l-205	ENSMUST00000196568.4	2681	No protein	Retained intron	-	-	TSL:1
Ubap2l-216	ENSMUST00000199016.1	2396	No protein	Retained intron	-	-	TSL:NA
Ubap2l-218	ENSMUST00000199301.1	2318	No protein	Retained intron	-	-	TSL:1
Ubap2l-214	ENSMUST00000198282.1	2271	No protein	Retained intron	-	-	TSL:1
Ubap2l-207	ENSMUST00000196747.1	2099	No protein	Retained intron	-	-	TSL:NA
Ubap2l-212	ENSMUST00000197633.1	1490	No protein	Retained intron	-	-	TSL:NA
Ubap2l-210	ENSMUST00000196952.1	1398	No protein	Retained intron	-	-	TSL:NA
Ubap2l-223	ENSMUST00000200301.1	620	No protein	Retained intron	-	-	TSL:3
Ubap2l-222	ENSMUST00000200195.1	479	No protein	Retained intron	-	-	TSL:3

The strategy is based on the design of *Ubap2l-202* transcript,The transcription is shown below

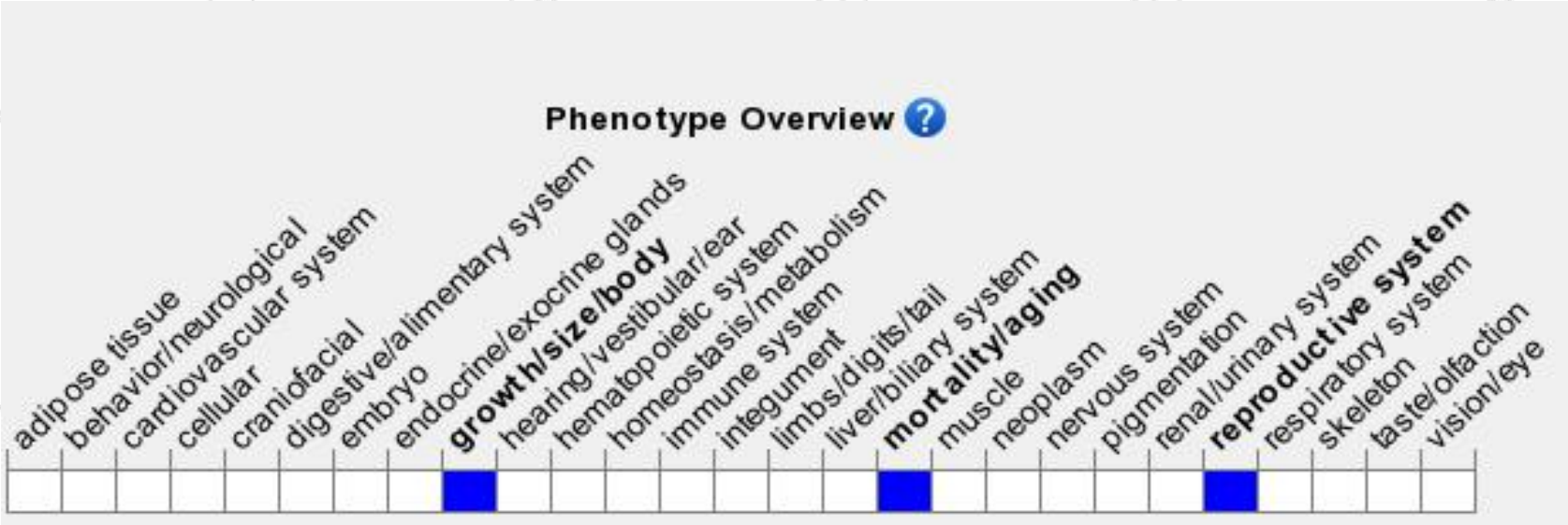
Genomic location distribution



Protein domain



Mouse phenotype description(MGI)



Phenotypes affected by the gene are marked in blue.Data quoted from MGI database(http://www.informatics.jax.org/).

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集萃药康
GemPharmatech

If you have any questions, you are welcome to inquire.

Tel: 400-9660890

集萃药康生物科技
GemPharmatech Co.,Ltd